

EYLER

#6

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/170,980

DATE: 12/14/1999
TIME: 03:21:43

INPUT SET: S34206.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Hillman, Jennifer L.
6 Goli, Surya K.
7
8 (ii) TITLE OF THE INVENTION: A NOVEL PROSTATE-ASSOCIATED
9 KALLIKREIN
10
11 (iii) NUMBER OF SEQUENCES: 4
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/170,980
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/790,137
34 (B) FILING DATE:
35
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Billings, Lucy J.
39 (B) REGISTRATION NUMBER: 36,749
40 (C) REFERENCE/DOCKET NUMBER: PF-0195 US
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 415-855-0555
44 (B) TELEFAX: 415-845-4166
45
46 (2) INFORMATION FOR SEQ ID NO:1:

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47

48

(i) SEQUENCE CHARACTERISTICS:

49

(A) LENGTH: 262 amino acids

50

(B) TYPE: amino acid

51

(C) STRANDEDNESS: single

52

(D) TOPOLOGY: linear

53

54

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

56

57

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly

58

1 5 10 15

59

Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu

60

20 25 30

61

Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe

62

35 40 45

63

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala

64

50 55 60

65

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu

66

65 70 75 80

67

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe

68

85 90 95

69

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln

70

100 105 110

71

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu

72

115 120 125

73

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr

74

130 135 140

75

Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser

76

145 150 155 160

77

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Leu Gln Cys Val Asp

78

165 170 175

79

Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys

80

180 185 190

81

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp

82

195 200 205

83

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu

84

210 215 220

85

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys

86

225 230 235 240

87

Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp

88

245 250 255

89

Thr Ile Ala Glu Asn Ser

90

260

91

92

(2) INFORMATION FOR SEQ ID NO:2:

93

94

(i) SEQUENCE CHARACTERISTICS:

95

(A) LENGTH: 833 base pairs

96

(B) TYPE: nucleic acid

97

(C) STRANDEDNESS: single

98

(D) TOPOLOGY: linear

99

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100
101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
102
103      GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC GCCCTGTCCC      60
104      TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC TGGGAGTGTG      120
105      AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCAGAA GACGCGGCTA CTCTGTGGGG      180
106      CGACGNTCAT NGCCCCCAGA TGGTTCCTGA CAGCAGCCCA CTGCCCTNAAG CCCCCTACA      240
107      TAGTTCACCT GGGGCAGCAC AACCTCCAGA AGGAGGAGGG CTGTGAGCAG ACCCGGACAG      300
108      CCACTGAGTC CTTCCCCCAC CCCGGCTTCA ACAACAGCCT CCCCAACAAA GACCACCGCA      360
109      ATGACATCAT GCTGGTGAAG ATGGCATCGC CAGTCTCCAT CACCTGGGCT GTGCGACCCC      420
110      TCACCCTCTC CTCACGCTGT GTCACCTGCTG GCACCAGCTG CCTCATTTCC GGTGTTGGGCA      480
111      GCACGTCCAG CCCCCAGTTA CGCCTGCCTC ACACCTTGCG ATGCGCCAAC ATCACCATCA      540
112      TTGAGCACCA GAAGTGTGAG AACGCCTACC CCGGCAACAT CACAGACACC ATGGTGTGTG      600
113      CCAGCGTGCA GGAAGGGGGC AAGGACTCCT GCCAGGGTGA CTCCGGGGGC CCTCTGGTCT      660
114      GTAACCAGTC TCTTCAAGGC ATTATCTCCT GGGGCCAGGA TCCGTGTGCG ATCACCCGAA      720
115      AGCCTGGTGT CTACACGAAA GTCTGCAAT ATGTGGACTG GATCCAGGAG ACGATGAAGA      780
116      ACAATTAGAC TGGACNTCAC CTCCGAANCC CCCACAGCCC ATCACCTCC ATT      833
117

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 186653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

131
132      Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
133      1          5          10          15
134      Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
135      20          25          30
136      Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
137      35          40          45
138      Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
139      50          55          60
140      His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
141      65          70          75          80
142      Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
143      85          90          95
144      Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
145      100         105         110
146      Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
147      115         120         125
148      Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
149      130         135         140
150      Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
151      145         150         155         160
152      Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp

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153
154      165      170      175
154      Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys
155      180      185      190
156      Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
157      195      200      205
158      Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
159      210      215      220
160      Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
161      225      230      235      240
162      Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
163      245      250      255
164      Thr Ile Ala Glu Asn Ser
165      260

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 55527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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180
181      Met Trp Phe Leu Ile Leu Phe Leu Ala Leu Phe Leu Gly Gly Ile Asp
182      1      5      10      15
183      Ala Ala Pro Pro Val Gln Ser Arg Ile Gly Gly Phe Asn Cys Glu
184      20      25      30
185      Lys Asn Ser Gln Pro Trp His Val Ala Val Tyr Arg Phe Ala Arg Tyr
186      35      40      45
187      Gln Cys Gly Gly Val Leu Leu Asp Ala Asn Trp Val Leu Thr Ala Ala
188      50      55      60
189      His Cys Tyr Asn Asp Lys Tyr Gln Val Trp Leu Gly Lys Asn Asn Arg
190      65      70      75      80
191      Phe Glu Asp Glu Pro Ser Ala Gln His Gln Leu Ile Ser Lys Ala Ile
192      85      90      95
193      Pro His Pro Gly Phe Asn Met Ser Leu Leu Asn Lys Asp His Thr Pro
194      100      105      110
195      His Pro Glu Asp Asp Tyr Ser Asn Asp Leu Met Leu Val Arg Leu Lys
196      115      120      125
197      Lys Pro Ala Glu Ile Thr Asp Val Val Lys Pro Ile Asp Leu Pro Thr
198      130      135      140
199      Glu Glu Pro Thr Val Gly Ser Arg Cys Leu Ala Ser Gly Trp Gly Ser
200      145      150      155      160
201      Thr Thr Pro Thr Glu Glu Phe Glu Tyr Ser His Asp Leu Gln Cys Val
202      165      170      175
203      Tyr Leu Glu Leu Leu Ser Asn Glu Val Cys Ala Lys Ala His Thr Glu
204      180      185      190
205      Lys Val Thr Asp Thr Met Leu Cys Ala Gly Glu Met Asp Gly Gly Lys

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RAW SEQUENCE LISTING
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/170,980

DATE: 12/14/1999
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INPUT SET: S34206.raw

Line	Error	Original Text
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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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DATE: 12/14/1999
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INPUT SET: S34206.raw

Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
8	(ii) TITLE OF THE INVENTION: A NOVEL PROSTATE	(ii) TITLE OF INVENTION: A NOVEL PROSTATE-ASS